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#2   OIPE

RAW SEQUENCE LISTING   DATE: 09/21/2001
PATENT APPLICATION: US/09/943,334   TIME: 20:46:45

Input Set : A:\tcs411div1.txt
Output Set: N:\CRF3\09212001\I943334.raw   ENTERED

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   3 <110> APPLICANT: Rittershaus, Charles W.
   4        Thomas, Lawrence J.
   6 <120> TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP)
ACTIVITY
   8 <130> FILE REFERENCE: TCS-411.1P US-1; Tcs-411.1P US-2
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/943,334
  11 <141> CURRENT FILING DATE: 2001-08-30
  13 <150> PRIOR APPLICATION NUMBER: 08/432,483
  14 <151> PRIOR FILING DATE: 1995-05-01
  16 <150> PRIOR APPLICATION NUMBER: PCT/US96/06147
  17 <151> PRIOR FILING DATE: 1996-05-01
  19 <150> PRIOR APPLICATION NUMBER: 08/945,289
  20 <151> PRIOR FILING DATE: 1997-10-17
  22 <160> NUMBER OF SEQ ID NOS: 9
  24 <170> SOFTWARE: PatentIn version 3.1
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  27 <211> LENGTH: 26
  28 <212> TYPE: PRT
  29 <213> ORGANISM: Artificial Sequence
  31 <220> FEATURE:
  32 <223> OTHER INFORMATION: C - terminal 26 amino acids of Human CETP
  34 <400> SEQUENCE: 1
  36 Arg Asp Gly Phe Leu Leu Leu Gln Met Asp Phe Gly Phe Pro Glu His
  37 1               5                   10                  15
  40 Leu Leu Val Asp Phe Leu Gln Ser Leu Ser
  41             20                  25
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  45 <211> LENGTH: 31
  46 <212> TYPE: PRT
  47 <213> ORGANISM: Artificial Sequence
  49 <220> FEATURE:
  50 <223> OTHER INFORMATION: vaccine peptide of the invention
  52 <400> SEQUENCE: 2
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  55 1               5                   10                  15
  58 Gly Phe Pro Glu His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser
  59             20                  25                  30
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  63 <211> LENGTH: 21
  64 <212> TYPE: PRT
  65 <213> ORGANISM: Artificial Sequence
  67 <220> FEATURE:
  68 <223> OTHER INFORMATION: helper T cell epitope of tetanus toxin
  70 <400> SEQUENCE: 3
  72 Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser
  73 1               5                   10                  15
  76 Ala Ser His Leu Glu
  77             20
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81 <211> LENGTH: 476
82 <212> TYPE: PRT
83 <213> ORGANISM: Homo Sapiens
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88 1   5   10   15
91 Lys Pro Ala Leu Leu Val Leu Asn His Glu Thr Ala Lys Val Ile Gln
92   20   25   30
95 Thr Ala Phe Gln Arg Ala Ser Tyr Pro Asp Ile Thr Gly Glu Lys Ala
96   35   40   45
99 Met Met Leu Leu Gly Gln Val Lys Tyr Gly Leu His Asn Ile Gln Ile
100   50   55   60
103 Ser His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Glu Ala Lys
104 65   70   75   80
107 Ser Ile Asp Val Ser Ile Gln Asn Val Ser Val Val Phe Lys Gly Thr
108   85   90   95
111 Leu Lys Tyr Gly Tyr Thr Thr Ala Trp Trp Leu Gly Ile Asp Gln Ser
112   100   105   110
115 Ile Asp Phe Glu Ile Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Gln
116   115   120   125
119 Leu Thr Cys Asp Ser Gly Arg Val Arg Thr Asp Ala Pro Asp Cys Tyr
120   130   135   140
123 Leu Ser Phe His Lys Leu Leu Leu His Leu Gln Gly Glu Arg Glu Pro
124 145   150   155   160
127 Gly Trp Ile Lys Gln Leu Phe Thr Asn Phe Ile Ser Phe Thr Leu Lys
128   165   170   175
131 Leu Val Leu Lys Gly Gln Ile Cys Lys Glu Ile Asn Val Ile Ser Asn
132   180   185   190
135 Ile Met Ala Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp
136   195   200   205
139 Gly Asp Ile Gly Val Asp Ile Ser Leu Thr Gly Asp Pro Val Ile Thr
140   210   215   220
143 Ala Ser Tyr Leu Glu Ser His His Lys Gly His Phe Ile Tyr Lys Asn
144 225   230   235   240
147 Val Ser Glu Asp Leu Pro Leu Pro Thr Phe Ser Pro Thr Leu Leu Gly
148   245   250   255
151 Asp Ser Arg Met Leu Tyr Phe Trp Phe Ser Glu Arg Val Phe His Ser
152   260   265   270
155 Leu Ala Lys Val Ala Phe Gln Asp Gly Arg Leu Met Leu Ser Leu Met
156   275   280   285
159 Gly Asp Glu Phe Lys Ala Val Leu Glu Thr Trp Gly Phe Asn Thr Asn
160   290   295   300
163 Gln Glu Ile Phe Gln Glu Val Val Gly Gly Phe Pro Ser Gln Ala Gln
164 305   310   315   320
167 Val Thr Val His Cys Leu Lys Met Pro Lys Ile Ser Cys Gln Asn Lys
168   325   330   335
171 Gly Val Val Val Asn Ser Ser Val Met Val Lys Phe Leu Phe Pro Arg
172   340   345   350

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175 Pro Asp Gln Gln His Ser Val Ala Tyr Thr Phe Glu Glu Asp Ile Val
176         355             360             365
179 Thr Thr Val Gln Ala Ser Tyr Ser Lys Lys Lys Leu Phe Leu Ser Leu
180     370             375             380
183 Leu Asp Phe Gln Ile Thr Pro Lys Thr Val Ser Asn Leu Thr Glu Ser
184 385             390             395             400
187 Ser Ser Glu Ser Ile Gln Ser Phe Leu Gln Ser Met Ile Thr Ala Val
188         405             410             415
191 Gly Ile Pro Glu Val Met Ser Arg Leu Glu Val Val Phe Thr Ala Leu
192         420             425             430
195 Met Asn Ser Lys Gly Val Ser Leu Phe Asp Ile Ile Asn Pro Glu Ile
196         435             440             445
199 Ile Thr Arg Asp Gly Phe Leu Leu Leu Gln Met Asp Phe Gly Phe Pro
200     450             455             460
203 Glu His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser
204 465             470             475
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207 <210> SEQ ID NO: 5
208 <211> LENGTH: 1428
209 <212> TYPE: DNA
210 <213> ORGANISM: Homo Sapiens
212 <400> SEQUENCE: 5
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215 ctggtgttga accacgagac tgccaaggtg atccagaccg ccttccagcg agccagctac     120
217 ccagatatca cgggcgagaa ggccatgatg ctccttggcc aagtcaagta tgggttgcac     180
219 aacatccaga tcagccactt gtccatcgcc agcagccagg tggagctggt ggaagccaag     240
221 tccattgatg tctccattca gaacgtgtct gtggtcttca aggggaccct gaagtatggc     300
223 tacaccactg cctggtggct gggtattgat cagtccattg acttcgagat cgactctgcc     360
225 attgacctcc agatcaacac acagctgacc tgtgactctg gtagagtgcg gaccgatgcc     420
227 cctgactgct acctgtcttt ccataagctg ctcctgcatc tccaagggga gcgagagcct     480
229 gggtggatca agcagctgtt cacaaatttc atctccttca ccctgaagct ggtcctgaag     540
231 ggacagatct gcaaagagat caacgtcatc tctaacatca tggccgattt tgtccagaca     600
233 agggctgcca gcatcctttc agatggagac attggggtgg acatttccct gacaggtgat     660
235 cccgtcatca cagcctccta cctggagtcc catcacaagg gtcatttcat ctacaagaat     720
237 gtctcagagg acctccccct ccccaccttc tcgcccacac tgctggggga ctcccgcatg     780
239 ctgtacttct ggttctctga gcgagtcttc cactcgctgg ccaaggtagc tttccagqat     840
241 ggccgcctca tgctcagcct gatgggagac gagttcaagg cagtgctgga gacctggggr     900
243 ttcaacacca accaggaaat cttccaagag gttgtcggcg gcttccccag ccaggcccaa     960
245 gtcaccgtcc actgcctcaa gatgcccaag atctcctgcc aaaacaaggg agtcgtggtc    1020
247 aattcttcag tgatggtgaa attcctcttt ccacgcccag accagcaaca ttctgtagct    1080
249 tacacatttg aagaggatat cgtgactacc gtccaggcct cctattctaa gaaaaagctc    1140
251 ttcttaagcc tcttggattt ccagattaca ccaaagactg tttccaactt gactgagagc    1200
253 agctccgagt ccatccagag cttcctgcag tcaatgatca ccgctgtggg catccctgag    1260
255 gtcatgtctc ggctcgaggt agtgtttaca gccctcatga acagcaaagg cgtgagcctc    1320
257 ttcgacatca tcaaccctga gattatcact cgagatggct cctgctgct gcagatggac    1380
259 tttggcttcc ctgagcacct gctggtggat ttcctccaga gcttgagc                1428
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262 <210> SEQ ID NO: 6
263 <211> LENGTH: 496
264 <212> TYPE: PRT
265 <213> ORGANISM: rabbit
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269 Cys Pro Lys Gly Ala Ser Tyr Glu Ala Gly Ile Val Cys Arg Ile Thr
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273 Lys Pro Ala Leu Leu Val Leu Asn Gln Glu Thr Ala Lys Val Val Gln
274             20                  25                  30
277 Thr Ala Phe Gln Arg Ala Gly Tyr Pro Asp Val Ser Gly Glu Arg Ala
278         35                  40                  45
281 Val Met Leu Leu Gly Arg Val Lys Tyr Gly Leu His Asn Leu Gln Ile
282     50                  55                  60
285 Ser His Leu Ser Ile Ala Ser Ser Gln Val Glu Leu Val Asp Ala Lys
286 65                  70                  75                  80
289 Thr Ile Asp Val Ala Ile Gln Asn Val Ser Val Val Phe Lys Gly Thr
290             85                  90                  95
293 Leu Asn Tyr Ser Tyr Thr Ser Ala Trp Gly Leu Gly Ile Asn Gln Ser
294             100                 105                 110
297 Val Asp Phe Glu Ile Asp Ser Ala Ile Asp Leu Gln Ile Asn Thr Glu
298         115                 120                 125
301 Leu Thr Cys Asp Ala Gly Ser Val Arg Thr Asn Ala Pro Asp Cys Tyr
302     130                 135                 140
305 Leu Ala Phe His Lys Leu Leu Leu His Leu Gln Gly Glu Arg Glu Pro
306 145                 150                 155                 160
309 Gly Trp Leu Lys Gln Leu Phe Thr Asn Phe Ile Ser Phe Thr Leu Lys
310             165                 170                 175
313 Leu Ile Leu Lys Arg Gln Val Cys Asn Glu Ile Asn Thr Ile Ser Asn
314             180                 185                 190
317 Ile Met Ala Asp Phe Val Gln Thr Arg Ala Ala Ser Ile Leu Ser Asp
318     195                 200                 205
321 Gly Asp Ile Gly Val Asp Ile Ser Val Thr Gly Ala Pro Val Ile Thr
322     210                 215                 220
325 Ala Thr Tyr Leu Glu Ser His His Lys Gly His Phe Thr His Lys Asn
326 225                 230                 235                 240
329 Val Ser Glu Ala Phe Pro Leu Arg Ala Phe Pro Pro Gly Leu Leu Gly
330             245                 250                 255
333 Asp Ser Arg Met Leu Tyr Phe Trp Phe Ser Asp Gln Val Leu Asn Ser
334             260                 265                 270
337 Leu Ala Arg Ala Ala Phe Gln Glu Gly Arg Leu Val Leu Ser Leu Thr
338     275                 280                 285
341 Gly Asp Glu Phe Lys Lys Val Leu Glu Thr Gln Gly Phe Asp Thr Asn
342     290                 295                 300
345 Gln Glu Ile Phe Gln Glu Leu Ser Arg Gly Leu Pro Thr Gly Gln Ala
346 305                 310                 315                 320
349 Gln Val Ala Val His Cys Leu Lys Val Pro Lys Ile Ser Cys Gln Asn
350             325                 330                 335
353 Arg Gly Val Val Val Ser Ser Ser Val Ala Val Thr Phe Arg Phe Pro
354             340                 345                 350
357 Arg Pro Asp Gly Arg Glu Ala Val Ala Tyr Arg Phe Glu Glu Asp Ile
358         355                 360                 365
361 Ile Thr Thr Val Gln Ala Ser Tyr Ser Gln Lys Lys Leu Phe Leu His
362     370                 375                 380
```

```
365 Leu Leu Asp Phe Gln Cys Val Pro Ala Ser Gly Arg Ala Gly Ser Ser
366 385                 390                 395                 400
369 Ala Asn Leu Ser Val Ala Leu Arg Thr Glu Ala Lys Ala Val Ser Asn
370                 405                 410                 415
373 Leu Thr Glu Ser Arg Ser Glu Ser Leu Gln Ser Ser Leu Arg Ser Leu
374                 420                 425                 430
377 Ile Ala Thr Val Gly Ile Pro Glu Val Met Ser Arg Leu Glu Val Ala
378             435             440             445
381 Phe Thr Ala Leu Met Asn Ser Lys Gly Leu Asp Leu Phe Glu Ile Ile
382         450             455             460
385 Asn Pro Glu Ile Ile Thr Leu Asp Gly Cys Leu Leu Leu Gln Met Asp
386 465             470             475             480
389 Phe Gly Phe Pro Lys His Leu Leu Val Asp Phe Leu Gln Ser Leu Ser
390             485             490             495
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394 <211> LENGTH: 1488
395 <212> TYPE: DNA
396 <213> ORGANISM: rabbit

398 <400> SEQUENCE: 7
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403 ccggacgtca gcggcgagag ggccgtgatg ctcctcggcc gggtcaagta cgggctgcac     180
405 aacctccaga tcagccacct gtccatcgcc agcagccagg tggagctggt ggacgccaag     240
407 accatcgacg tcgccatcca gaacgtgtcc gtggtcttca aggggaccct gaactacagc     300
409 tacacgagtg cctggggggtt gggcatcaat cagtctgtcg acttcgagat cgactctgcc     360
411 attgacctcc agatcaacac agagctgacc tgcgacgctg gcagtgtgcg caccaatgcc     420
413 cccgactgct acctggcttt ccataaactg ctcctgcacc tccagggggga gcgcgagccg     480
415 gggtggctca agcagctctt cacaaacttc atctccttca ccctgaagct gattctgaag     540
417 cgacaggtct gcaatgagat caacaccatc tccaacatca tggctgactt tgtccagacg     600
419 agggccgcca gcatcctctc agatggagac atcggggtgg acatttccgt gacggggggcc     660
421 cctgtcatca cagccaccta cctggagtcc catcacaagg gtcacttcac gcacaagaac     720
423 gtctccgagg ccttccccct ccgcgccttc ccgcccggtc ttctgggggga ctcccgcatg     780
425 ctctacttct ggttctccga tcaagtgctc aactccctgg ccaggccgc cttccaggag     840
427 ggccgtctcg tgctcagcct gacaggggat gagttcaaga aagtgctgga gacccagggt     900
429 ttcgacacca accaggaaat cttccaggag ctttccagag gccttcccac cggccaggcc     960
431 caggtagccg tccactgcct taaggtgccc aagatctcct gccagaaccg gggtgtcgtg    1020
433 gtgtcttctt ccgtcgccgt gacgttccgc ttcccccgcc cagatggccg agaagctgtg    1080
435 gcctacaggt ttgaggagga tatcatcacc accgtccagg cctcctactc ccagaaaaag    1140
437 ctcttcctac acctcttgga tttccagtgc gtgccggcca gcggaagggc aggcagctca    1200
439 gcaaatctct ccgtggccct caggactgag gctaaggct tttccaacct gactgagagc    1260
441 cgctccgagt ccctgcagag ctctctccgc tccctgatcg ccacggtggg catcccggag    1320
443 gtcatgtctc ggctcgaggt ggcgttcaca gccctcatga acagcaaagg cctggacctc    1380
445 ttcgaaatca tcaaccccga gattatcact ctcgatggct gcctgctgct gcagatggac    1440
447 ttcggttttc ccaagcacct gctggtggat ttcctgcaga gcctgagc               1488
450 <210> SEQ ID NO: 8
451 <211> LENGTH: 50
452 <212> TYPE: PRT
453 <213> ORGANISM: Artificial Sequence

455 <220> FEATURE:
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/943,334

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number